

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2001, 15:30:32 ; Search time 23.63 Seconds
(Without alignments) 658.146 Million cell updates/sec

Title: US-09-653-755A-4

Perfect score: 2427
Sequence: 1 EVQLOOSGELVKPGASVMI.....RHEGLKNYTKTKTISPKK 454

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1802	74.2	306	1 GCB_MOUSE	P01866 mus musculus
2	1797	74.0	405	1 GCBM_MOUSE	P01867 mus musculus
3	1419	58.5	330	1 GCAA_MOUSE	P01863 mus musculus
4	1414	58.3	399	1 GCAB_MOUSE	P01864 mus musculus
5	1385.5	57.1	335	1 GCB_MOUSE	P01864 mus musculus
6	1326.5	54.7	333	1 GCB_MOUSE	P01864 mus musculus
7	1202.5	49.5	329	1 GCB_MOUSE	P01864 mus musculus
8	1170	48.2	329	1 GCB_MOUSE	P01864 mus musculus
9	1159	47.8	398	1 GCB_MOUSE	P01864 mus musculus
10	1150	47.4	324	1 GCB_MOUSE	P01864 mus musculus
11	1145	47.2	393	1 GCB_MOUSE	P01864 mus musculus
12	1112	45.8	326	1 GCB_MOUSE	P01864 mus musculus
13	1100	45.3	322	1 GCB_MOUSE	P01864 mus musculus
14	1087	44.8	330	1 GCB_MOUSE	P01864 mus musculus
15	1080.5	44.5	323	1 GCB_MOUSE	P01864 mus musculus
16	1080.5	44.5	323	1 GCB_MOUSE	P01864 mus musculus
17	1059	43.6	326	1 GCB_MOUSE	P01864 mus musculus
18	1054.5	43.4	327	1 GCB_MOUSE	P01864 mus musculus
19	776.5	32.0	290	1 GCB_MOUSE	P01864 mus musculus
20	478	19.7	454	1 GCB_MOUSE	P01864 mus musculus
21	477.5	19.7	429	1 GCB_MOUSE	P01864 mus musculus
22	474	19.5	421	1 GCB_MOUSE	P01864 mus musculus
23	473	19.5	428	1 GCB_MOUSE	P01864 mus musculus
24	462	19.0	118	1 GCB_MOUSE	P01864 mus musculus
25	457.5	18.9	117	1 GCB_MOUSE	P01864 mus musculus
26	457.5	18.9	117	1 GCB_MOUSE	P01864 mus musculus
27	443.5	18.3	438	1 GCB_MOUSE	P01864 mus musculus
28	436.5	18.0	370	1 GCB_MOUSE	P01864 mus musculus
29	431.5	17.8	438	1 GCB_MOUSE	P01864 mus musculus
30	431	17.8	139	1 GCB_MOUSE	P01864 mus musculus
31	430.5	17.7	120	1 GCB_MOUSE	P01864 mus musculus
32	430.5	17.7	120	1 GCB_MOUSE	P01864 mus musculus
33	429.5	17.7	136	1 GCB_MOUSE	P01864 mus musculus

ALIGNMENTS

RESULT	1	STANDARD	PRT	336 AA
GCB_MOUSE				
ID	GCB_MOUSE			
AC	P01866;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	IG GAMMA-2B CHAIN C REGION.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_Taxid:10090;			
RN	[1]			
RP	SEQUENCE FROM N.A. (A ALLELE)			
RX	MEDLINE-80120716; PubMed-6766534;			
RA	Yanawaki-Kataoka Y., Kataoka T., Takahashi N., Odata M., Honjo T.;			
RT	"Complete nucleotide sequence of immunoglobulin gamma2b chain gene			
RT	cloned from newborn mouse DNA.";			
RL	Nature 283:786-789(1980).			
RN	[2]			
RP	SEQUENCE FROM N.A. (MPC 11).			
RX	MEDLINE-80081501; PubMed-117548;			
RA	Tucker P.W., Marcu K.B., Slightom J.L., Blattner F.R.;			
RT	"Structure of the constant and 3' untranslated regions of the murine			
RT	gamma 2b heavy chain messenger RNA.";			
RL	Science 206:1299-1303(1979).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-80081502; PubMed-117549;			
RA	Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;			
RT	"Sequence of the cloned gene for the constant region of murine gamma			
RT	2b immunoglobulin heavy chain.";			
RL	Science 206:1303-1306(1979).			
RN	[4]			
RP	SEQUENCE FROM N.A. (B ALLELE)			
RX	MEDLINE-82173203; PubMed-6803173;			
RA	Olio R., Rougeon F.;			
RT	"Mouse immunoglobulin allotypes: post-duplication divergence of gamma			
RT	2a and gamma 2b chain genes.";			
RL	Nature 296:761-763(1982).			
RN	[5]			
RP	CARBOHYDRATE-LINKAGE SITE THR-105.			
RX	MEDLINE-94216359; PubMed-7512967;			
RA	Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K.;			
RT	Irimura T., Takahashi N., Kato K., Arata Y.;			
RT	"O-glycosylation in hinge region of mouse immunoglobulin G2b.";			
RL	J. Biol. Chem. 269:12345-12350(1994).			
CC	-1- PM: O-LINKED GLYCANS CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH IS			
CC	MODIFIED WITH 2 SIALIC ACID RESIDUES.			
CC	-1- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLOG WITH OTHER IG GAMMA			
CC	CHAINS.			
CC	-1- MISCELLANEOUS: THE A ALLELE SEQUENCE IS SHOWN.			
DR	PIR: A02157; GZMS11.			
DR	InterPro: IPR000495; -			
DR	InterPro: IPR003006; -			
DR	Pfam: PF00047; 1g; 3.			

DR PROSITE: PS00290; IG-MHC: 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT NON-TER 1 1 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 15 15
 FT DISULFID 27 82
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 150 210
 FT DISULFID 256 314
 FT CARBOHYD 105 105
 FT MOD-RES 336 336
 FT VARIANT 163 163
 FT VARIANT 194 194
 FT VARIANT 300 300
 FT VARIANT 301 301
 FT CONFLICT 25 25
 FT CONFLICT 36 36
 FT CONFLICT 239 239
 SQ SEQUENCE 336 AA: 36658 MW: 78879662607C356E CRC64;

Query Match 74.2%; Score 1802; DB 1; Length 336;
 Best Local Similarity 100.0%; Pred. No. 1,3e-118;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 119 AKTTPSVYPLAPGCGDITGSSVTLGCLVKGYPESVYVYTNMNGSLSSVHPFPALLOSG 178
 DB 1 AKTTPSVYPLAPGCGDITGSSVTLGCLVKGYPESVYVYTNMNGSLSSVHPFPALLOSG 60
 OY 179 LYTMSSTVTPSPSTPSTQVTCVSAHPASTTVDKRLKLESPGISTINPCPPCKECHKCPA 238
 DB 61 LYTMSSTVTPSPSTPSTQVTCVSAHPASTTVDKRLKLESPGISTINPCPPCKECHKCPA 120
 OY 239 PNLGEGPSVFIPPNKIDVLMISLPKVTQVVDVSEDDPDQVISMVFNNEVHTAQOT 298
 DB 121 PNLGEGPSVFIPPNKIDVLMISLPKVTQVVDVSEDDPDQVISMVFNNEVHTAQOT 180
 OY 299 HREDYNSITRVVSTLPIDQHDMMGSKERKCKVNNKDLSPRIETRTISKIGLVARPOVYIL 358
 DB 181 HREDYNSITRVVSTLPIDQHDMMGSKERKCKVNNKDLSPRIETRTISKIGLVARPOVYIL 240
 OY 359 PPAPQLSKDVSLTCLVGVFNPBGDISVEMTNGHTEENYKDTAPVLDSDGSYFYISKLN 418
 DB 241 PPAPQLSKDVSLTCLVGVFNPBGDISVEMTNGHTEENYKDTAPVLDSDGSYFYISKLN 300
 OY 419 MKTSKWEKTDSPSCNVRHGLKNYIKRTISRPCK 454
 DB 301 MKTSKWEKTDSPSCNVRHGLKNYIKRTISRPCK 336

RESULT 2
 GCBM_MOUSE
 ID GCBM_MOUSE STANDARD; PRT: 405 AA.
 AC 01867;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-2H CHAIN C REGION, MEMBRANE-BOUND FORM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE OF 335-405 FROM N.A.
 RA MEDLINE=82222190; PubMed=6283537;
 RA Yamawaki-Ratacka Y., Nakai S., Miyata T., Honjo T.;
 RT "Nucleotide sequences of gene segments encoding membrane domains of
 RL immunoglobulin gamma chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 RP SEQUENCE OF 335-378 FROM N.A.

RX MEDLINE=82115295; PubMed=6799207;
 RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
 RA Eisenberg D., Wall R.;
 RT "Gene segments encoding transmembrane carboxyl termini of
 RT immunoglobulin gamma chains.";
 RL Cell 26:19-27(1981).
 CC -I- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
 CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
 CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
 CC BOUND CHAINS. IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
 CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
 CC SEGMENT OF MU CHAINS.
 CC -I- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA
 CC CHAINS.
 CC -I- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-335 IS ASSUMED TO BE
 CC IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM.
 CC -I- MISCELLANEOUS: THE A ALLELE SEQUENCE IS SHOWN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: J00462; AAB59659.1; ALT_INIT.
 CC PIR: C02154; G2MSBM.
 CC MGI: MGI:96445; Igh-3.
 CC InterPro: IPR000495; -;
 CC DR Pfam: PF00047; 19; 3.
 CC DR PROSITE: PS00290; IG-MHC: 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Transmembrane;
 KW Alternative splicing;
 FT NON-TER 1 1
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 82
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 150 210
 FT DISULFID 256 314
 FT TRANSMEM 352 369
 FT DOMAIN 370 405
 SQ SEQUENCE 405 AA: 44330 MW: 89B3CF0A5B6D9FA CRC64;
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).

Query Match 74.0%; Score 1797; DB 1; Length 405;
 Best Local Similarity 100.0%; Pred. No. 3,6e-118;
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 119 AKTTPSVYPLAPGCGDITGSSVTLGCLVKGYPESVYVYTNMNGSLSSVHPFPALLOSG 178
 DB 1 AKTTPSVYPLAPGCGDITGSSVTLGCLVKGYPESVYVYTNMNGSLSSVHPFPALLOSG 60
 OY 179 LYTMSSTVTPSPSTPSTQVTCVSAHPASTTVDKRLKLESPGISTINPCPPCKECHKCPA 238
 DB 61 LYTMSSTVTPSPSTPSTQVTCVSAHPASTTVDKRLKLESPGISTINPCPPCKECHKCPA 120
 OY 239 PNLGEGPSVFIPPNKIDVLMISLPKVTQVVDVSEDDPDQVISMVFNNEVHTAQOT 298
 DB 121 PNLGEGPSVFIPPNKIDVLMISLPKVTQVVDVSEDDPDQVISMVFNNEVHTAQOT 180
 OY 299 HREDYNSITRVVSTLPIDQHDMMGSKERKCKVNNKDLSPRIETRTISKIGLVARPOVYIL 358
 DB 181 HREDYNSITRVVSTLPIDQHDMMGSKERKCKVNNKDLSPRIETRTISKIGLVARPOVYIL 240
 OY 359 PPAPQLSKDVSLTCLVGVFNPBGDISVEMTNGHTEENYKDTAPVLDSDGSYFYISKLN 418
 DB 241 PPAPQLSKDVSLTCLVGVFNPBGDISVEMTNGHTEENYKDTAPVLDSDGSYFYISKLN 300

[illegible]

FT	DISULFID	27	82	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	107	107	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	110	110	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	112	112	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	144	204	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	250	308	INTERCHAIN (WITH A HEAVY CHAIN).
FT	MOD. RES	330	330	INTERCHAIN (WITH A HEAVY CHAIN).
SO	SEQUENCE	330 AA;	36389 MM;	REMOVED POST-TRANSLATIONALLY.
				B04361C54456864 CXC64;
	Query Match	58.5%;	Score 1419;	DB 1; Length 330;
	Best Local Similarity	78.6%;	Pred. No. 5.9e-92;	
	Matches 264;	Conservative 30;	Mismatches 36;	Indels 6; Gaps 2;
OY	119	AKTTPSYVPLAPGCGDGTGGSSVLTGCLYKGYFPSPSVYTNWNSGLSSSVHTFPALDSG	178	
DB	1	AKTTPSYVPLAPGCGDGTGGSSVLTGCLYKGYFPSPSVYTNWNSGLSSSVHTFPALDSG	60	
OY	179	LYTMSSTVTPSSPMSQVTCNVANHPASSSTVDKRLKESGISTINPCPPCKECHKCPA	238	
DB	61	LYTMSSTVTPSSPMSQVTCNVANHPASSSTVDKRLKESGISTINPCPPCKECHKCPA	114	
OY	239	PNLGSGPVFTFPPIKIKVLMISLTPKTYCVVADVSEDDPDVQISMFVNNVHTAQTQT	298	
DB	115	PNLGSGPVFTFPPIKIKVLMISLTPKTYCVVADVSEDDPDVQISMFVNNVHTAQTQT	174	
OY	299	HREDYNSTIRVYSTLPIDIOHDMMSKREKCKVNNKDLSPERTISKIKGLVAPQVYL	358	
DB	175	HREDYNSTIRVYSTLPIDIOHDMMSKREKCKVNNKDLSPERTISKIKGLVAPQVYL	234	
OY	359	PPPAQSLSRKQVSLCLVGVFNPGDISVEMTNSNGHTEENKRTAVLDSDSGYFIYSKLN	418	
DB	235	PPPEEMKMKQVTLICMVTDFEMPEDIYEWMTNNGTEENKRTAVLDSDSGYFIYSKLN	294	
OY	419	MKTSKEKTDSPSCNVRRHGELKNYILKTYITISRPCK	454	
DB	295	VEKKMVERNSTYCSVVAHGLNHHHTTSFSKTPCK	330	
	RESULT	4		
	GCAM_MOUSE	STANDARD:	PRT:	399 AA.
AC	P01865:			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	IG GAMMA-2A CHAIN C REGION, MEMBRANE-BOUND FORM.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RA	SEQUENCE FROM N.A.			
RA	MEDLINE=82222190; PubMed=6283537;			
RT	Yamawaki-Katoka Y., Nakai S., Miyata T., Honjo T.;			
RT	"Nucleotide sequences of gene segments encoding membrane domains of			
RT	immunoglobulin gamma chains.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).			
CC	-I- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA			
CC	SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED			
CC	GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-			
CC	BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED			
CC	IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND			
CC	SEGMENT OF MU CHAINS.			
CC	-I- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE			
CC	IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF			
CC	THE A ALLELE.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR EMBL: J00471; AAB59661.1; ALT_INIT.

DR PIR: A02154; G2MSAB.

DR MGI: 966443; Igh-1.

DR InterPro: IPR000495; -.

DR InterPro: IPR003006; -.

DR Pfam: PF00047; Iq; 3.

DR PROSITE: PS00290; IG_MHC; 1.

KM Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

Transmembrane; Alternative splicing.

FT NON_TER 1 1

FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 144 204

FT DISULFID 250 308

FT TRANSMEM 346 363

FT DOMAIN 364 399

FT CARBOHYD 180 180

FT SEQUENCE 399 AA; 44020 MW; 4C38138BFAED3FF0 CRC64;

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLUCNAC...) (POTENTIAL).

Query Match 58.3%; Score 1414; DB 1; Length 399;

Best local similarity 78.5%; Pred. No. 1.7e-91;

Matches 263; Conservative 30; Mismatches 36; Indels 6; Gaps 2;

QY 119 AKTTPSVYPLACGDDTSSVTLCGLVKGYPESVYTWNSGLSSSVHFPALLOSG 178

DB 1 AKTTPSVYPLACGDDTSSVTLCGLVKGYPESVYTWNSGLSSSVHFPALLOSG 60

QY 179 LYTMSSSVYPPSTSPQVTCVAHPASTYDKKLEPESGISTINPCPKCKECHKCPA 238

DB 61 LYTMSSSVYPPSTSPQVTCVAHPASTYDKKLEPESGISTINPCPKCKECHKCPA 114

QY 239 PNLGGPSVFIFPPNKKDVLMIATPKVTCVYVDSEDDPDVQISWVNNVEVHTAQOT 298

DB 115 PNLGGPSVFIFPPNKKDVLMIATPKVTCVYVDSEDDPDVQISWVNNVEVHTAQOT 174

QY 299 HREDYSTRVAVSTLPIQHODMMSGKEFKCKVNNKDLPSPIERTISKIGLYRAPQVYL 358

DB 175 HREDYSTRVAVSTLPIQHODMMSGKEFKCKVNNKDLPSPIERTISKIGLYRAPQVYL 234

QY 359 PPAEOLSKRDVSLTCLVYGFNPDISVEWTSNGHTEENKOTAPVLDSDGSYFIYSKLN 418

DB 235 PPAEOLSKRDVSLTCLVYGFNPDISVEWTSNGHTEENKOTAPVLDSDGSYFIYSKLN 294

QY 419 MKTSKWEKTDSEFCNVRHGLKNYLYLKTISRSPG 453

DB 295 VEKKNNVERNSYSCSVYHGLNHNHTTKSRIRPG 329

RESULT 5

GCAB_MOUSE STANDARD: PRT: 335 AA.

AC P01864:

DT 21-JUL-1986 (rel. 01, Created)

DT 21-JUL-1986 (rel. 01, Last sequence update)

DT 15-JUL-1999 (rel. 38, Last annotation update)

DE IG GAMMA-2A CHAIN C REGION, B ALLELE.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

SEQUENCE FROM N.A.

RP STRAIN=C57BL/6;

RX MEDLINE=82037861; PubMed=6170065;

RA Schreier P.H., Botwell A.L.M., Mueller-Hill B., Baltimore D.;

RT "Multiple differences between the nucleic acid sequences of the

RT IgG2a and IgG2b alleles of the mouse.";

Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).

RN [2]

RP SEQUENCE

RA MEDLINE=82037777; PubMed=6794027;

RA Dognin M.J., Lauwereys M., Strosberg A.D.;

RT "Multiple amino acid substitutions between murine gamma 2a heavy

chain Fc regions of Ig1a and Ig1b allotypic forms.";

Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).

CC - MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,

FROM BALB/C MICE, AT 158 OF THE POSITIONS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

or send an email to license@isb-sib.ch).

CC EMBL: J00479; -; NOT_ANNOTATED_CDS.

DR PIR: A02153; G2MSAB.

DR InterPro: IPR000495; -.

DR InterPro: IPR003006; -.

DR Pfam: PF00047; Iq; 3.

DR PROSITE: PS00290; IG_MHC; 1.

KM Immunoglobulin domain; Immunoglobulin C region.

FT NON_TER 1 1

FT SEQUENCE 335 AA; 36596 MW; FA3382792CB13C6 CRC64;

Query Match 57.1%; Score 1385.5; DB 1; Length 335;

Best local similarity 77.1%; Pred. No. 1.3e-89;

Matches 259; Conservative 33; Mismatches 43; Indels 1; Gaps 1;

QY 119 AKTTPSVYPLACGDDTSSVTLCGLVKGYPESVYTWNSGLSSSVHFPALLOSG 178

DB 1 AKTTPSVYPLACGDDTSSVTLCGLVKGYPESVYTWNSGLSSSVHFPALLOSG 60

QY 179 LYTMSSSVYPPSTSPQVTCVAHPASTYDKKLEPESGISTINPCPKCKECHKCPA 238

DB 61 LYTMSSSVYPPSTSPQVTCVAHPASTYDKKLEPESGISTINPCPKCKECHKCPA 119

QY 239 PNLGGPSVFIFPPNKKDVLMIATPKVTCVYVDSEDDPDVQISWVNNVEVHTAQOT 298

DB 120 PNLGGPSVFIFPPNKKDVLMIATPKVTCVYVDSEDDPDVQISWVNNVEVHTAQOT 179

QY 299 HREDYSTRVAVSTLPIQHODMMSGKEFKCKVNNKDLPSPIERTISKIGLYRAPQVYL 358

DB 180 HREDYSTRVAVSTLPIQHODMMSGKEFKCKVNNKDLPSPIERTISKIGLYRAPQVYL 239

QY 359 PPAEOLSKRDVSLTCLVYGFNPDISVEWTSNGHTEENKOTAPVLDSDGSYFIYSKLN 418

DB 240 PPAEOLSKRDVSLTCLVYGFNPDISVEWTSNGHTEENKOTAPVLDSDGSYFIYSKLN 299

QY 419 MKTSKWEKTDSEFCNVRHGLKNYLYLKTISRSPG 454

DB 300 VQKSTWERSLFCACSVYHGLNHNHTTKISRSLK 335

RESULT 6

GCAB_MOUSE STANDARD: PRT: 333 AA.

AC P20761:

DT 01-FEB-1991 (rel. 17, Created)

DT 01-FEB-1991 (rel. 17, Last sequence update)

DT 15-JUL-1999 (rel. 38, Last annotation update)

DE IG GAMMA-2B CHAIN C REGION.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=892323738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family";
RL Gene 74:473-482(1988).
DR PIR; PS0018; PS0018.
DR InterPro; IPR000495; -
DR InterPro; IPR003006; -
DR Pfam; PF00047; 1g; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 54.7%; Score 1326.5; DB 1; Length 333;
Best Local Similarity 73.6%; Pred. No. 1.6e-85;
Matches 248; Conservative 34; Mismatches 50; Indels 5; Gaps 3;

QY 119 AKTTPSVYPLAPGCGDGTSSVTGLCLVKGYFPEPSVTYVNWNSGLSSVHTFPALLQSG 178
1 AQTAPSVYPLAPGCGDGTSSVTGLCLVKGYFPEPSVTYVNWNSGLSSVHTFPALLQSG 60
DB 1 LYTSSSVTVSSVMPSTQVTCVAHPASSSTTVDKKLE-PSGPSTINPCPPCKCHKCP 237
179 LYTSSSVTVSSVMPSTQVTCVAHPASSSTTVDKKLE-PSGPSTINPCPPCKCHKCP 237
DB 61 LYTSSSVTVSSVMPSTQVTCVAHPASSSTTVDKKLE-PSGPSTINPCPPCKCHKCP 116
238 APNLEGGSVFIFPPNIDVIMISLTPKVCYVVDVEDDPOVQSMFVNNEVHTAQTQ 297
DB 117 VPELLGGSVFIFPPKPKDILLISQNAKVTCCVVDSEEDPOVQSMFVNNEVHTAQTQ 176
QY 298 THREDYNTIRVSTLPIQHODMMSGKEFKCKVNNKDLPSPIERTISKIGLVRAQYVI 357
177 PREEDYNTIRVSTLPIQHODMMSGKEFKCKVNNKDLPSPIERTISKIGLVRAQYVI 236
DB 358 LPPEAQSLKRDVSLTCLVGFNPEDISVEWTSNGHTEENYKDPAPVLDSDGSYFIYSKL 417
237 MGPPEAQSLKRDVSLTCLVGFNPEDISVEWTSNGHTEENYKDPAPVLDSDGSYFIYSKL 296
QY 418 MKTSKWEKTDSPSCNVRHEGLKNYLLKKTISRSPGK 454
297 NVERSKWDSPAPFCVYHEGLAHNHVKSISRSPGK 333
DB

RESULT 7
GCC_RAT
ID GCC_RAT STANDARD; PRT; 329 AA.
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-2C CHAIN C REGION.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86166903; PubMed=3127222;
RA Brueggemann M., Delmastro-Galiffe P., Waldmann H., Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
region cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:317-319(1988).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb.ch/announcement/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07189; CAA30169.1; -
DR PIR; S00847; S00847.
DR InterPro; IPR000495; -
DR InterPro; IPR003006; -
DR Pfam; PF00047; 1g; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 222 CH2.
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCDD7B7933850773 CRC64;

Query Match 49.5%; Score 1202.5; DB 1; Length 329;
Best Local Similarity 68.2%; Pred. No. 7e-77;
Matches 229; Conservative 35; Mismatches 65; Indels 7; Gaps 4;

QY 119 AKTTPSVYPLAPGCGDGTSSVTGLCLVKGYFPEPSVTYVNWNSGLSSVHTFPALLQSG 178
1 ARTTAPSVYPLAPGCGDGTSSVTGLCLVKGYFPEPSVTYVNWNSGLSSVHTFPALLQSG 60
DB 179 LYTSSSVTVSSVMPSTQVTCVAHPASSSTTVDKKLE-PSGPSTINPCPPCKCHKCP 238
61 LYTSSSVTVSSVMPSTQVTCVAHPASSSTTVDKKLE-PSGPSTINPCPPCKCHKCP 114
QY 239 PNLEGGSVFIFPPNIDVIMISLTPKVCYVVDVEDDPOVQSMFVNNEVHTAQTQ 298
115 DNL-GRPSVFIFPPKPKDILLISQNAKVTCCVVDSEEDPOVQSMFVNNEVHTAQTQ 173
DB 299 HREDYNTIRVSTLPIQHODMMSGKEFKCKVNNKDLPSPIERTISKIGLVRAQYVI 358
174 HEEQNGTFRVSTLPIQHODMMSGKEFKCKVNNKDLPSPIERTISKIGLVRAQYVI 233
QY 359 PPPAEQSLKRDVSLTCLVGFNPEDISVEWTSNGHTEENYKDPAPVLDSDGSYFIYSKL 418
234 PPPAEQSLKRDVSLTCLVGFNPEDISVEWTSNGHTEENYKDPAPVLDSDGSYFIYSKL 293
DB 419 MKTSKWEKTDSPSCNVRHEGLKNYLLKKTISRSPGK 454
294 VDTDSWNRGDIYTCSVYHEALHNHTQKNLSRSPGK 329
DB

RESULT 8
GCC_MOUSE
ID GCC_MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-3 CHAIN C REGION, SECRETED FORM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.D., Rimm D., Der-Balan G.P., Martinez H.M.,

```

RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RN EMBL J. 3:2041-2046(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: J00451; NOT_ANNOTATED_CDS.
DR PIR: B02156; G3MSC.
DR InterPro: IPR000495; -.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 3.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin C region; Glycoprotein; Transmembrane;
KW Alternative splicing.
FT NON_TER 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 48.2%; Score 1170; DB 1; Length 329;
Best Local Similarity 66.2%; Pred. No. 1.3e-74;
Matches 221; Conservative 33; Mismatches 74; Indels 6; Gaps 1;

QY 121 TTPPSVYPLAPGCGDTGSSVTLGCLVKGYFPEPSVYVWNSSGSLSSVHTFPALLQSGLY 180
DB 2 TTPPSVYPLAPGCGSDTSSGSSVTLGCLVKGYFPEPSVYVWNSSGSLSSVHTFPALLQSGLY 61
QY 181 TMSSTVTVSSSTWSPQTVCSVAHPASSTVDKLEPSGPISTINPCPPCKECHKCPAPN 240
DB 62 SLSSLVTVSSSTWSPQTVCSVAHPASSTVDKLEPSGPISTINPCPPCKECHKCPAPN 115
QY 241 LGGPSVFETFPKPKDLMISLTPKVTGVVVDSEDDPDVHSMFVDNKEVHTAMTQPRE 300
DB 116 ILGGPSVFETFPKPKDLMISLTPKVTGVVVDSEDDPDVHSMFVDNKEVHTAMTQPRE 175
QY 301 EDYNSIRVYSLTPIQHOHMSGKEFKCKVNNKDLPSPIERTISKIGLVRAPOVYITLP 360
DB 176 AQYNSIFRVYSLTPIQHOHMSGKEFKCKVNNKDLPSPIERTISKIGLVRAPOVYITLP 235
QY 361 PAEOLSRKDVSLTCLVGVGNPDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLANK 420
DB 236 PREOMSKKKVSLTCLVGNPDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLANK 295
QY 421 TSKWEKTDSEFCNVNRHEGLKNTYLLKTTISRSPCK 454
DB 296 TDSWLQGEIFTCVYVHEALHNHTQKNLSRSPCK 329

RESULT 9
GC3M_MOUSE STANDARD; PRT; 398 AA.
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-3 CHAIN C REGION, MEMBRANE-BOUND FORM.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,

```

```

RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RN EMBL J. 3:2041-2046(1984).
CC [2]
CC SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE=84041483; PubMed=6314258;
RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
RT segment.";
CC Nucleic Acids Res. 11:6775-6785(1983).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: J00451; AAB59655.1; ALT_SEQ.
DR PIR: A02156; G3MSM.
DR InterPro: IPR000495; -.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 3.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT TRANSMEM 346 362 POTENTIAL.
FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 398 AA; 43929 MW; CF7E264B50A41B95 CRC64;

Query Match 47.8%; Score 1159; DB 1; Length 398;
Best Local Similarity 66.0%; Pred. No. 9.5e-74;
Matches 219; Conservative 33; Mismatches 74; Indels 6; Gaps 1;

QY 121 TTPPSVYPLAPGCGDTGSSVTLGCLVKGYFPEPSVYVWNSSGSLSSVHTFPALLQSGLY 180
DB 2 TTPPSVYPLAPGCGSDTSSGSSVTLGCLVKGYFPEPSVYVWNSSGSLSSVHTFPALLQSGLY 61
QY 181 TMSSTVTVSSSTWSPQTVCSVAHPASSTVDKLEPSGPISTINPCPPCKECHKCPAPN 240
DB 62 SLSSLVTVSSSTWSPQTVCSVAHPASSTVDKLEPSGPISTINPCPPCKECHKCPAPN 115
QY 241 LGGPSVFETFPKPKDLMISLTPKVTGVVVDSEDDPDVHSMFVDNKEVHTAMTQPRE 300
DB 116 ILGGPSVFETFPKPKDLMISLTPKVTGVVVDSEDDPDVHSMFVDNKEVHTAMTQPRE 175
QY 301 EDYNSIRVYSLTPIQHOHMSGKEFKCKVNNKDLPSPIERTISKIGLVRAPOVYITLP 360
DB 176 AQYNSIFRVYSLTPIQHOHMSGKEFKCKVNNKDLPSPIERTISKIGLVRAPOVYITLP 235
QY 361 PAEOLSRKDVSLTCLVGVGNPDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLANK 420
DB 236 PREOMSKKKVSLTCLVGNPDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLANK 295
QY 421 TSKWEKTDSEFCNVNRHEGLKNTYLLKTTISRSP 452
DB 296 TDSWLQGEIFTCVYVHEALHNHTQKNLSRSP 327

RESULT 10
GC1_MOUSE

```

```

ID GC1_MOUSE STANDARD; PRT; 324 AA.
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE IG GAMMA-1 CHAIN C REGION.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Ohta M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT gamma 1 chain gene.";
RL Cell 18:559-568(1979).
[2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE=80202559; PubMed=6769752;
RA Ohta M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
RT cloned in a bacterial plasmid.";
RL Gene 9:87-97(1980).
[3]
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=80012837; PubMed=113776;
RA Rogers J., Clarke P., Salsner W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
RT heavy chain.";
RL Nucleic Acids Res. 6:3305-3321(1979).
[4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=78242288; PubMed=98524;
RA Adeltubo K.;
RT "Evolution of immunoglobulin subclasses. Primary structure of a
RT murine myeloma gamma1 chain.";
RL J. Biol. Chem. 253:6068-6075(1978).
[5]
RP DISULFIDE BONDS (MOPC 21).
RX MEDLINE=73008889; PubMed=5073237;
RA Swastl J., Milstien C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL Biochem. J. 126:837-850(1972).
-----
CC CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
EMBL: V00793; CAA24172.1; -
EMBL: V00793; CAA24173.1; -
EMBL: V00793; CAA24174.1; -
EMBL: V00793; CAA24175.1; -
EMBL: V00795; CAA24176.1; -
PIR: A02159; G1MS.
DR Glycosylated; P01868; -
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR000495; -
DR InterPro; IPR003006; -
DR Pfam; PF00047; Iq; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW alternative splicing.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.

```

```

FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT CARBOHYD 138 198 N-LINKED (GLCNAC. . .).
FT CARBOHYD 174 174
FT DISULFID 244 302
FT MOD_RES 324 324 REMOVED POST-TRANSLATIONALLY.
FT CONFLICT 276 276 N -> D (IN REF. 3).
FT CONFLICT 278 278 N -> D (IN REF. 3).
SO SEQUENCE 324 AA; 35704 MW; A338812P3D1F2C93 CRC64;

Query Match 47.48; Score 1150; DB 1; Length 324;
Best local similarity 64.68; Pred. No. 3.1e-73;
Matches 217; Conservative 45; Mismatches 62; Indels 12; Gaps 4;

QY 119 AKTPPSVYPLAPGCGDTGSSVTLGCLYKGFPEPSVYVWNSGSLSSVTFPVALDQSG 178
DB 1 AKTPPSVYPLAPGSAQTNSMVTGLCYGFPEPVYVWNSGSLSSGVTFPVALDQSD 60
QY 179 LYTMSSTVYPSSTWPSQTVTCVAHPASSTVYDKLEPSSGPISTINPCPCCKCHKCPA 238
DB 61 LYTSSSTVYPSSPRSTETVCNVAHPASSVYDKLTP-----RDC-GCKPC-ICTV 111
QY 239 PNLGGDSVFLEFPNIKDVLMISLTPKVTGVVDVSEDDPVDQISVFNVEVHTPAQTOT 298
DB 112 PEVS---SVFLEPPKPKDVLITLTPKVTGVVDISKDDPEVQSWFVDVEVHTAQTQ 168
QY 299 HREDYNGTIRVSLPLPIOHOMNSGKEFKCKVNNKDLPSLPIERTISIKGLVRAPOVYIL 358
DB 169 REQFNSTFRSVSELPIMHOMLNGKEFKCRVNSAAPAPLEKTSIKGGRKAPQVYTI 228
QY 359 PPPEQLSRKDVSLTCLVYVGNPGDISVETNSNGHTEWTSKDTFAPVLDSDSYFLSKLN 418
DB 229 PPPEQMAKDKVSLTCAITTFDFPEDIYEMQNKQAPENYNTQPIANTNGSYFLSKLN 288
QY 419 MKTSKWEKTDSPSCNVRHEGLKNYYLKKTTISRSBQK 454
DB 289 VQKSNWEAGNFTCSVLHEGLHNHTEKLSHSPGK 324

RESULT 11
GC1_MOUSE STANDARD; PRT; 393 AA.
ID GC1_MOUSE
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE IG GAMMA-1 CHAIN C REGION. MEMBRANE-BOUND FORM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Ohta M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT gamma 1 chain gene.";
RL Cell 18:559-568(1979).
[2]
RP SEQUENCE OF 323-393 FROM N.A.
RX MEDLINE=82197626; PubMed=6804950;
RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT "mRNA for surface immunoglobulin gamma chains encodes a highly
RT conserved transmembrane sequence and a 28-residue intracellular
RT domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
[3]

```


RP SEQUENCE OF 323-366 FROM N.A.
 RA MEDLINE=82115295; PubMed=6799207;
 RX ROGERS J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
 RA Eisenberg D., Wall R.;
 RT "Gene segments encoding transmembrane carboxyl termini of
 RT immunoglobulin gamma chains.";
 RL Cell 26:19-27(1981).
 RN [4]
 RP SEQUENCE OF 1-44 FROM N.A.
 RX MEDLINE=8222190; PubMed=6283537;
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
 RT "Nucleotide sequences of gene segments encoding membrane domains of
 RT immunoglobulin gamma chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 CC -I- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
 CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
 CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
 CC BOUND CHAINS. IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
 CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
 CC SEGMENT OF MU CHAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: V00793; CAA24172.1;
 DR EMBL: V00793; CAA24173.1;
 DR EMBL: V00793; CAA24174.1;
 DR PIR: B02159; GIMSM.
 DR MGD: MGI:96446; Igh-4.
 DR InterPro: IPR000495;
 DR InterPro: IPR003006;
 DR Pfam: PF00047; Ig; 3.
 DR ProSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Alternative splicing; Transmembrane.
 FT NON-TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 110 HINGE.
 FT DOMAIN 111 217 CH2.
 FT DOMAIN 218 324 CH3.
 FT DISULFID 27 82
 FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 138 198
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
 FT DISULFID 244 302
 FT TRANSMEM 340 357
 FT DOMAIN 358 393 POTENTIAL.
 FT SEQUENCE 393 AA; 43386 MW; 4CC8343B7A1CE27 CRC64; CYTOPLASMIC (POTENTIAL).
 Query Match 47.2%; Score 1145; DB 1; Length 393;
 Best Local Similarity 64.5%; Pred. No. 8.8e-73;
 Matches 216; Conservative 45; Mismatches 62; Indels 12; Gaps 4;
 QY 119 AKTTPPSVYPLAPGCGDPTGSSVTLGCLVKGYPESVYVYTNSSGSSSVHTFPALDSG 178
 DB 1 AKTTPPSVYPLAPGSAQNSMTLGLCLVKGYPPEVYVYTNSSGSSSVHTFPALDSG 60
 QY 179 LYTMSSTVTPSPSTQVTCVSAHPASTVYDKKLEPSCGISTINPCPPCKECHKCPA 238
 DB 61 LYTLLSSVTPSPSPSTQVTCVSAHPASTVYDKKLEPSCGISTINPCPPCKECHKCPA 238
 QY 239 PNLGEGPSVFIFPPPIKIDVLMISLPKVTGVVVDVSEDDPDVQISMFVNNVEVHTAQTOT 298
 DB 112 PEVSV---SVFIFPPKPKVDLTITLPKVTGVVVDVSKDDPEVQISMFVNDVDEVHTAQTOT 168

QY 299 HREDYNSITRVSTLPIQHODMWSGKEFKCKVNNKDLPSPIERTISKIGLVARPOVYL 358
 DB 169 REBQFNSTRSVSELPIMQDMLNGKEFKCRVNSAFAPIPIERTISKIGRKAQOVYI 228
 QY 359 PPPEQLSRKDYSLCLVGVGPNPGDISVEMTSNGHTEENYKDTAPVLDSDGSFYISKLN 418
 DB 229 PPKPEQMARKDYSLTCMDTFEPEDITEVMQNGQPAENYKKTOTPIMTNNGSYFYISKLN 288
 QY 419 MKTSKWEKTDSPSCNVRHGLKNYIKRTISRSPG 453
 DB 289 VQKSNMEAGNFTCVSLHGLHNHTEKLSHSPG 323
 RESULT 12
 ID GCL_RAT STANDARD; PRT; 326 AA.
 AC P20759;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-1 CHAIN C REGION.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8232738; PubMed=3149946;
 RA Brueggemann M.;
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
 RL Gene 74:473-482(1988).
 DR PIR: PS0017; PS0017.
 DR InterPro: IPR000495;
 DR InterPro: IPR003006;
 DR Pfam: PF00047; Ig; 3.
 DR ProSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT NON-TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 112 HINGE.
 FT DOMAIN 113 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 27 82
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;
 Query Match 45.8%; Score 1112; DB 1; Length 326;
 Best Local Similarity 61.9%; Pred. No. 1.4e-70;
 Matches 208; Conservative 50; Mismatches 68; Indels 10; Gaps 3;
 QY 119 AKTTPPSVYPLAPGCGDPTGSSVTLGCLVKGYPESVYVYTNSSGSSSVHTFPALDSG 178
 DB 1 AKTTPPSVYPLAPGSAQNSMTLGLCLVKGYPPEVYVYTNSSGSSSVHTFPALDSG 60
 QY 179 LYTMSSTVTPSPSTQVTCVSAHPASTVYDKKLEPSCGISTINPCPPCKECHKCPA 238
 DB 61 LYTLLSSVTPSPSPSTQVTCVSAHPASTVYDKKLEPSCGISTINPCPPCKECHKCPA 238
 QY 239 PNLGEGPSVFIFPPPIKIDVLMISLPKVTGVVVDVSEDDPDVQISMFVNNVEVHTAQTOT 298
 DB 114 SEVSV---SVFIFPPKPKVDLTITLPKVTGVVVDVSKDDPEVHFMVVDVDEVHTAQTOT 170
 QY 299 HREDYNSITRVSTLPIQHODMWSGKEFKCKVNNKDLPSPIERTISKIGLVARPOVYL 358
 DB 171 PEEGNSITRVSTLPIQHODMWSGKEFKCKVNNKDLPSPIERTISKIGLVARPOVYL 230

RT "Rule of antibody structure. The primary structure of a monoclonal
 RT 19G1 immunoglobulin (myeloma protein M μ), I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanoagen bromide cleavage products, and the disulfide bridges."
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE-81208100; PubMed-7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9 and 2.8-A resolution."
 RL Biochemistry 20:2361-2370(1981).
 CC -I- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE
 CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
 CC MARKER & THE GIM (NON-1) MARKERS.
 CC -I- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35,116,198,269 & 272.
 CC -I- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155,166,177,195,198,269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -I- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198,267&272.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J00228; AAC82527.1; ALT_INIT.
 DR PIR: A02146; GHU.
 DR PDB: 1RC1; 15-JUL-92.
 DR PDB: 1RC2; 15-JUL-92.
 DR MIM: 147100;
 DR InterPro: IPR000495;
 DR InterPro: IPR003006;
 DR Pfam: PF00047; 19; 3.
 DR PROSITE: PS00290; IG_MHC. 2.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW 3D-structure.
 FT NON_TER 1 1
 FT DOMAIN 99 110 CH1.
 FT DOMAIN 111 223 HINGE.
 FT DOMAIN 224 330 CH2.
 FT DISULFID 27 83 CH3.
 FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 144 204 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 250 308
 FT CARBOHYD 180 180
 FT MOD_RES 330 330
 FT VARIANT 97 97
 FT VARIANT 239 239
 FT VARIANT 241 241
 FT STRAND 123 126
 FT HELIX 130 134
 FT TURN 136 137
 FT STRAND 141 148
 FT STRAND 158 162
 FT TURN 163 164
 FT STRAND 165 166
 FT STRAND 175 178
 FT STRAND 183 190
 FT HELIX 193 197
 FT TURN 198 199
 N-LINKED (GLCNAC. . .).
 REMOVED POST-TRANSLATIONALLY.
 K -> R (IN GIM(3) MARKER).
 D -> E (IN GIM(NON-1) MARKER).
 /FTID-VAR_003886.
 L -> M (IN GIM(NON-1) MARKER).
 /FTID-VAR_003888.

FT STRAND 202 206
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT HELIX 238 240
 FT TURN 241 242
 FT STRAND 245 256
 FT STRAND 260 266
 FT TURN 267 268
 FT STRAND 269 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT TURN 302 303
 FT STRAND 306 312
 FT TURN 313 314
 FT TURN 316 317
 FT STRAND 320 324
 SO SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA3D CRC64;

 Query Match 44.8%; Score 1087; DB 1; Length 330;
 Best Local Similarity 60.8%; Pred. No. 7; 7e-69;
 Matches 205; Conservative 49; Mismatches 75; Indels 8; Gaps 3;

 QY 119 AKTPPSVYPLANGCDDTGGSSVTLCGLYKGPRESVTVTWNGSLSSVHTFPALLO-S 177
 DB 1 ASKQSVPLPSSKSTSGGTAALGLVKDYPPEVTVSWNGSLTSGVHTFPALQSS 60
 QY 178 GLTSSSVTVPSSTWSPQSVTCVAHPASSFTVDKLEPSPGISTINCPCKECKCP 237
 DB 61 GLXSLSSVTVPSSTSLGTQTYICNVHKNPSNTKVDKVERKSDKI-HICPP-----CP 113
 QY 238 APNLGGSPSVFTFPPIKQVLMISLTPKVTQVVDVSEDDPDVQISMFVNNVEVHTAQTO 297
 DB 114 APELLGGSPSVFTFPKPKDTLMISRPEVTCVVDVSHEDPEVKFMVYDGEVHNAKTK 173
 QY 298 THREDVNSTIRVSTLPPIQHOVMGSKERKCYNNKDLSPFIERTSKIKGLVRAQVYI 357
 DB 174 PREQYNSTIRVSVTLVTHQDLNKEKCYKSNALPAPLEKTISSKAKGPREQVYT 233
 QY 358 LPPAPQLSRKDVSLTCLVAVGPNPDISVEWTSNGHTEENYKDTAVLSDSSEYFYSKL 417
 DB 234 LPPSRBELTKNQVSLTCLYKGFPSDIAVEMESNGPENNKTTPVLDSDGSFLYSL 293
 QY 418 NMKTSKWEKTDSEFCNVRHDEGLKNYLLKRTISRPCK 454
 DB 294 TVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSPCK 330

 RESULT 15
 GC_RABIT STANDARD; PRT; 323 AA.
 AC P01870;
 DT 21-JUL-1986 (rel. 01, Created)
 DT 21-JUL-1986 (rel. 01, Last sequence update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE IG GAMMA CHAIN C REGION.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_Taxid=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-84030930; PubMed-6313520;
 RA Bernstein K.E., Alexander C.B., Mage R.G.;
 RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
 RL F-I haplotype."
 RL Immunogenetics 18:387-397(1983).
 RN [2]
 RP SEQUENCE OF 1-128.

RX MEDLINE=76135469; PubMed=1243651;
 RA Pratt D.M., Mole L.E.;
 RT "Sequence studies on the constant region of the Fd sections of rabbit
 RT Immunoglobulin G of different allotype.";
 RL Biochem. J. 151:337-349(1975).
 RN [3]
 RP SEQUENCE OF 88-266 FROM N.A.
 RX MEDLINE=83299917; PubMed=6193512;
 RA Matens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
 RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
 RT heavy chain and identification of two genomic C gamma genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
 RN [4]
 RP SEQUENCE OF 132-161.
 RX MEDLINE=70110015; PubMed=5461106;
 RA Frutcher R.G., Jackson S.A., Mole L.E., Porter R.R.;
 RT "Sequence studies of the Fd section of the heavy chain of rabbit
 RT Immunoglobulin G.";
 RL Biochem. J. 116:249-259(1970).
 RN [5]
 RP SEQUENCE OF 129-131 AND 155-322.
 RA Hill R.L., Leboyvitz H.E., Fellows R.E. Jr., Delaney R.;
 RL (In) Kiliander J. (eds.);
 RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
 RL Stockholm (1967).
 CC -I- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
 CC 104-THR. AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
 CC MARKERS AND REF.5 THE E15 MARKER.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M16426; AAA31289.1; -
 DR PIR: A02161; GHRB.
 DR InterPro: IPR000495; -
 DR InterPro: IPR003006; -
 DR Pfam: PF00047; 19; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 KM NOX_TER 1
 FT 1
 FT VARIANT 104 104 T -> M (IN D11 MARKER).
 FT VARIANT 185 185 T -> A (IN E15 MARKER).
 FT CONFLICT 48 48 N -> E (IN REF. 2).
 FT CONFLICT 71 71 V -> VPV (IN REF. 2).
 FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
 FT CONFLICT 173 173 N -> D (IN REF. 5).
 FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
 FT CONFLICT 201 201 N -> D (IN REF. 5).
 FT CONFLICT 218 218 Q -> E (IN REF. 5).
 FT CONFLICT 233 233 E -> Q (IN REF. 5).
 FT CONFLICT 246 246 N -> D (IN REF. 5).
 FT CONFLICT 256 256 E -> G (IN REF. 5).
 FT CONFLICT 260 260 N -> D (IN REF. 5).
 FT CONFLICT 266 266 N -> D (IN REF. 5).
 FT CONFLICT 280 280 Y -> W (IN REF. 5).
 FT CONFLICT 284 284 N -> S (IN REF. 5).
 SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 44.5%; Score 1080.5; DB 1; Length 323;
 Best Local Similarity 61.4%; Pred. No. 2,1e-68;
 Matches 205; Conservative 48; Mismatches 62; Indels 19; Gaps 4;

QY 124 PSYPLAPGCGDTGSSVTLGLVKGYPESVYVWNSGLSSSVHTFPALLQ-SGLYTM 182
 Db 6 PSVPLAPCCGDTSPSTLGLVKGYPESVYVWNSGLSSSVHTFPALLQ-SGLYTM 65
 QY 183 SSVTVPSSTWPSQTVCSVAHPASSTVVDKLEPSGPISTINPCPCKCHK--CPAPN 240

Db 66 SSVVSVTS---SQPYTCNVAAHPAINTKVDKTVAPS-----TCSKPTCPPE 109
 QY 241 LEGGDSVFIEPPNPKIDVIMISLTPRVTCVVVDSEDDPDVQISWFNVEVHTAQOTHR 300
 Db 110 LLGDSVAFIEPPPKPKDILMISRTPEVTCVVVDSDDEVOFTWYINNEQVTRAPPLRE 169
 QY 301 EDYNTIVVSTLPTQHODMMSGKEFKCKVNNKDLPSFIERISKIKGLVRAPOYIILP 360
 Db 170 QQFNSTIRVSTLPTTHODWLRGKEFKCKVNNKALPAPIEKTISKARQPLEPKYTMGP 229
 QY 361 PAEOLSRKDVSLTCLVVGFNPDISVWTSNGHEENYKDTAPVLDSDGSFYISKLNK 420
 Db 230 PRELLSSRSVSLTCLVVGFNPDISVWTSNGHEENYKDTAPVLDSDGSFYISKLNK 289
 QY 421 TSKMEKTDSESCNVRHKGKLYVYKKTTSRSPGK 454
 Db 290 TSEWQRGDVFTCSVWHEALHNHYTQKISRSPGK 323

Search completed: June 18, 2001, 15:34:34
 Job time: 242 sec

